

0590
1009#2
OICE

RAW SEQUENCE LISTING

DATE: 11/19/2001

PATENT APPLICATION: US/09/939,226

TIME: 08:52:05

Input Set : N:\Crf3\RULE60\09939226.raw

Output Set: N:\CRF3\11192001\I939226.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: SAMSON, MICHEL

6 PARMENTIER, MARC

7 VASSART, GILBERT

8 LIBERT, FREDERICK

10 (ii) TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR

11 AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

13 (iii) NUMBER OF SEQUENCES: 17

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Knobbe, Martens, Olson & Bear

17 (B) STREET: 620 Newport Center Drive 16th Floor

18 (C) CITY: Newport Beach

19 (D) STATE: CA

20 (E) COUNTRY: U.S.A.

21 (F) ZIP: 92660

ENTERED

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk

25 (B) COMPUTER: IBM PC compatible

26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/09/939,226

C--> 31 (B) FILING DATE: 24-Aug-2001

32 (C) CLASSIFICATION:

35 (vii) PRIOR APPLICATION DATA:

36 (A) APPLICATION NUMBER: 09/626,939

37 (B) FILING DATE: 2000-07-27

42 (viii) ATTORNEY/AGENT INFORMATION:

43 (A) NAME: Altman, Daniel E

44 (B) REGISTRATION NUMBER: 34,115

45 (C) REFERENCE/DOCKET NUMBER:

47 (2) INFORMATION FOR SEQ ID NO: 1:

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 792 base pairs

51 (B) TYPE: nucleic acid

52 (C) STRANDEDNESS: single

53 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: DNA (genomic)

58 (ix) FEATURE:

59 (A) NAME/KEY: CDS

60 (B) LOCATION: 240..791

63 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

65 GAATTCCCCC AACAGAGCCA AGCTCTCCAT CTAGTGGACA GGAAGCTAG CAGCAAACCT 60

66 TCCCTTCACT ACAAACCTTC ATTGCTTGGC CAAAAAGAGA GTTAATTCAA TGTAGACATC 120

67 TATGTAGGCA ATTAAAAACC TATTGATGTA TAAACAGTT TGCATTCATG GAGGGCAACT 180

68 AAATACATTC TAGGACTTTA TAAAGATCA CTTTTTATTT ATGCACAGGG TGAACAAG 239

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69 ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC ATC AAT TAT TAT ACA      287
70 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
71   1           5           10           15
72 TCG GAG CCC TGC CAA AAA ATC AAT GTG AAG CAA ATC GCA GCC CGC CTC      335
73 Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
74           20           25           30
75 CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT GGT TTT GTG GGC AAC      383
76 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
77           35           40           45
78 ATG CTG GTC ATC CTC ATC CTG ATA AAC TGC AAA AGG CTG AAG AGC ATG      431
79 Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
80   50           55           60
81 ACT GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT GAC CTG TTT TTC CTT      479
82 Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
83  65           70           75           80
84 CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC GCC CAG TGG GAC TTT      527
85 Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
86           85           90           95
87 GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC      575
88 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
89   100           105           110
90 TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG      623
91 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
92   115           120           125
93 GCT GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT      671
94 Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
95   130           135           140
96 GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GCT GTG TTT GCG TCT      719
97 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
98 145           150           155           160
99 CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC      767
100 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
101           165           170           175
102 ACC TGC AGC TCT CAT TTT CCA TAC A      792
103 Thr Cys Ser Ser His Phe Pro Tyr
104           180
107 (2) INFORMATION FOR SEQ ID NO: 2:
109   (i) SEQUENCE CHARACTERISTICS:
110       (A) LENGTH: 1477 base pairs
111       (B) TYPE: nucleic acid
112       (C) STRANDEDNESS: single
113       (D) TOPOLOGY: linear
115   (ii) MOLECULE TYPE: DNA (genomic)
118   (ix) FEATURE:
119       (A) NAME/KEY: CDS
120       (B) LOCATION: 240..1295
123   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
125 GAATTCCCCC AACAGAGCCA AGCTCTCCAT CTAGTGGACA GGGAAAGCTAG CAGCAAACCT      60
126 TCCCTTCACT ACAAACCTTC ATTGCTTGGC CAAAAAGAGA GTTAATTCAA TGTAGACATC      120

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127	TATGTAGGCA	ATTAAAAACC	TATTGATGTA	TAAAACAGTT	TGCATTCATG	GAGGGCAACT	180
128	AAATACATTC	TAGGACTTTA	TAAAAGATCA	CTTTTATTT	ATGCACAGGG	TGGAACAAG	239
129	ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC ATC AAT TAT TAT ACA	287					
130	Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr						
131	1 5 10 15						
132	TCG GAG CCC TGC CAA AAA ATC AAT GTG AAG CAA ATC GCA GCC CGC CTC	335					
133	Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu						
134	20 25 30						
135	CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT GGT TTT GTG GGC AAC	383					
136	Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn						
137	35 40 45						
138	ATG CTG GTC ATC CTC ATC CTG ATA AAC TGC AAA AGG CTG AAG AGC ATG	431					
139	Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met						
140	50 55 60						
141	ACT GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT GAC CTG TTT TTC CTT	479					
142	Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu						
143	65 70 75 80						
144	CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC GCC CAG TGG GAC TTT	527					
145	Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe						
146	85 90 95						
147	GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC	575					
148	Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe						
149	100 105 110						
150	TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG	623					
151	Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu						
152	115 120 125						
153	GCT GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT	671					
154	Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe						
155	130 135 140						
156	GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GCT GTG TTT GCG TCT	719					
157	Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser						
158	145 150 155 160						
159	CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC	767					
160	Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr						
161	165 170 175						
162	ACC TGC AGC TCT CAT TTT CCA TAC AGT CAG TAT CAA TTC TGG AAG AAT	815					
163	Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn						
164	180 185 190						
165	TTC CAG ACA TTA AAG ATA GTC ATC TTG GGG CTG GTC CTG CCG CTG CTT	863					
166	Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu						
167	195 200 205						
168	GTC ATG GTC ATC TGC TAC TCG GGA ATC CTA AAA ACT CTG CTT CGG TGT	911					
169	Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys						
170	210 215 220						
171	CGA AAT GAG AAG AAG AGG CAC AGG GCT GTG AGG CTT ATC TTC ACC ATC	959					
172	Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile						
173	225 230 235 240						
174	ATG ATT GTT TAT TTT CTC TTC TGG GCT CCC TAC AAC ATT GTC CTT CTC	1007					
175	Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu						

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176          245          250          255
177 CTG AAC ACC TTC CAG GAA TTC TTT GGC CTG AAT AAT TGC AGT AGC TCT      1055
178 Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser
179          260          265          270
180 AAC AGG TTG GAC CAA GCT ATG CAG GTG ACA GAG ACT CTT GGG ATG ACG      1103
181 Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr
182          275          280          285
183 CAC TGC TGC ATC AAC CCC ATC ATC TAT GCC TTT GTC GGG GAG AAG TTC      1151
184 His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe
185          290          295          300
186 AGA AAC TAC CTC TTA GTC TTC TTC CAA AAG CAC ATT GCC AAA CGC TTC      1199
187 Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
188 305          310          315          320
189 TGC AAA TGC TGT TCT ATT TTC CAG CAA GAG GCT CCC GAG CGA GCA AGC      1247
190 Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
191          325          330          335
192 TCA GTT TAC ACC CGA TCC ACT GGG GAG CAG GAA ATA TCT GTG GGC TTG      1295
193 Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu
194          340          345          350
195 TGACACGGAC TCAAGTGGGGC TGGTGACCCA GTCAGAGTTG TGCACATGGC TTAGTTTTTCA      1355
196 TACACAGCCT GGGCTGGGGG TNGGTTGGNN GAGGTCTTTT TTAAGAGGAA GTTACTGTTA      1415
197 TAGAGGGTCT AAGATTCATC CATTTATTTG GCATCTGTTT AAAGTAGATT AGATCCGAAT      1475
198 TC                                                                 1477
201 (2) INFORMATION FOR SEQ ID NO: 3:
203   (i) SEQUENCE CHARACTERISTICS:
204       (A) LENGTH: 1442 base pairs
205       (B) TYPE: nucleic acid
206       (C) STRANDEDNESS: single
207       (D) TOPOLOGY: linear
209   (ii) MOLECULE TYPE: DNA (genomic)
212   (ix) FEATURE:
213       (A) NAME/KEY: CDS
214       (B) LOCATION: 240..884
217   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
219 GAATTCCCCC AACAGAGCCA AGCTCTCCAT CTAGTGACCA GGGAAGCTAG CAGCAAACCT      60
220 TCCCTTCACT ACAAACCTTC ATTGCTTGGC CAAAAAGAGA GTTAATTCAA TGTAACATC      120
221 TATGTAGGCA ATTAAAAACC TATTGATGTA TAAACAGTT TGCATTCATG GAGGGCAACT      180
222 AAATACATTC TAGGACTTTA TAAAAGATCA CTTTTATTTT ATGCACAGGG TGGAAACAAG      239
223 ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC ATC AAT TAT TAT ACA      287
224 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
225 1          5          10          15
226 TCG GAG CCC TGC CAA AAA ATC AAT GTG AAG CAA ATC GCA GCC CGC CTC      335
227 Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
228          20          25          30
229 CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT GGT TTT GTG GGC AAC      383
230 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
231          35          40          45
232 ATG CTG GTC ATC CTC ATC CTG ATA AAC TGC AAA AGG CTG AAG AGC ATG      431
233 Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met

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Input Set : N:\Crf3\RULE60\09939226.raw

Output Set: N:\CRF3\11192001\I939226.raw

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234      50      55      60
235 ACT GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT GAC CTG TTT TTC CTT      479
236 Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
237 65      70      75      80
238 CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC GCC CAG TGG GAC TTT      527
239 Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
240      85      90      95
241 GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC      575
242 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
243      100      105      110
244 TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG      623
245 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
246      115      120      125
247 GCT GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT      671
248 Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
249      130      135      140
250 GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GCT GTG TTT GCG TCT      719
251 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
252 145      150      155      160
253 CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC      767
254 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
255      165      170      175
256 ACC TGC AGC TCT CAT TTT CCA TAC ATT AAA GAT AGT CAT CTT GGG GCT      815
257 Thr Cys Ser Ser His Phe Pro Tyr Ile Lys Asp Ser His Leu Gly Ala
258      180      185      190
259 GGT CCT GCC GCT GCT TGT CAT GGT CAT CTG CTA CTC GGG AAT CCT AAA      863
260 Gly Pro Ala Ala Cys His Gly His Leu Leu Leu Gly Asn Pro Lys
261      195      200      205
262 AAC TCT GCT TCG GTG TCG AAA TGAGAAGAAG AGGCACAGGG CTGTGAGGCT      914
263 Asn Ser Ala Ser Val Ser Lys
264      210      215
265 TATCTTCACC ATCATGATTG TTTATTTTCT CTTCTGGGCT CCCTACAACA TTGTCCTTCT      974
266 CCTGAACACC TTCCAGGAAT TCTTTGGCCT GAATAATTGC AGTAGCTCTA ACAGGTGGA      1034
267 CCAAGCTATG CAGGTGACAG AGACTCTTGG GATGACGCAC TGCTGCATCA ACCCATCAT      1094
268 CTATGCCTTT GTCGGGGAGA AGTTCAGAAA CTACCTCTTA GTCTTCTTCC AAAAGCACAT      1154
269 TGCCAAACGC TTCTGCAAAT GCTGTTCTAT TTTCCAGCAA GAGGCTCCCG AGCGAGCAAG      1214
270 CTCAGTTTAC ACCCGATCCA CTGGGGAGCA GGAAATATCT GTGGGCTTGT GACACGGACT      1274
271 CAAGTGGGCT GGTGACCCAG TCAGAGTTGT GCACATGGCT TAGTTTTTCAT ACACAGCCTG      1334
272 GGCTGGGGGT GGTGGGAGG TCTTTTTTAA AAGGAAGTTA CTGTTATAGA GGGTCTAAGA      1394
273 TTCATCCATT TATTTGGCAT CTGTTTAAAG TAGATTAGAT CCGAATTC      1442
276 (2) INFORMATION FOR SEQ ID NO: 4:
277 (i) SEQUENCE CHARACTERISTICS:
278 (A) LENGTH: 184 amino acids
279 (B) TYPE: amino acid
280 (D) TOPOLOGY: linear
281 (ii) MOLECULE TYPE: protein
282 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
283 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
284 1      5      10      15

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/939,226

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Output Set: N:\CRF3\11192001\I939226.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:418 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7
L:462 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:477 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8
L:509 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:521 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:536 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9
L:595 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10
L:617 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:639 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10